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Spatial Structures of PAP(262–270) and PAP(274–284), Two Selected Fragments of PAP(248–286), an Enhancer of HIV Infectivity

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Abstract

© 2015, Springer-Verlag Wien. Prostatic acid phosphatase (PAP) assembles into amyloid fibrils that facilitate infection by HIV. Its peptide fragments PAP(248–286) and PAP(85–120) also enhance attachment of the virus by viral adhesion to the host cell prior to receptor-specific binding via reducing the electrostatic repulsion between the membranes of the virus and the target cell. The secondary structure of monomeric PAP(248–286) in a biomembrane-mimicking environment can be separated into an N-terminal unordered region, an α-helical central domain, and an α/310-helical C-terminal section (Nanga et al., J. Am. Chem. Soc., 131:17972–17979, 2009). In this work, we used two-dimensional nuclear magnetic resonance (2D NMR) spectroscopy techniques to study spatial structures of isolated central [PAP(262–270)] and C-terminal [PAP(274–284)] fragments of PAP(248–286) in SDS micelle solutions. NMR studies revealed the formation of complexes of both peptides with SDS micelles, with attraction to the micelle membranes occurring mainly through nonpolar and uncharged residues of the peptides. We demonstrate that, when interacting with SDS micelles, PAP(262–270) and PAP(274–284) form α-helical and 310-helical secondary structures, respectively, similar to that found previously for the 39-residue PAP(248–286).

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